Application for UNITED STATES LETTERS PATENT

of

YOSHU YOSHIBA

KAZUKO SHINOZAKI

and

KAZUO SHINOZAKI

for

TRANSGENIC RICE PLANT AND ITS FAMILY WITH ENVIRONMENTAL STRESS RESISTANT BY PROLINE ACCUMULATION OF HIGH LEVEL AND ITS PRODUCTION

25

5

SPECIFICATION

TITLE OF THE INVENTION

Transgenic rice plant and its family with environmental stress resistant by proline accumulation of high level and its production

BACKGROUND OF THE INVENTION

The present invention relates to a rice plant having a high level of proline accumulating ability, and improved salinity-tolerance, drought-tolerance, and low temperature-tolerance, and its production method.

It is known that, for several plants including halophytes, when the plants are subjected to a high salinity stress or a drought stress, they accumulate proline, which is one of amino acids, in their cytoplasms. This is considered useful for regulating the osmotic pressure in the plant cytoplasm, or inhibiting the degradation of a functional protein due to the stress. The proline in a plant is synthesized from a glutamic acid by two enzymes of a Δ^1 -pyrroline-5-carboxylate (P5C) synthetase (P5CS) and a P5C reductase. On the other hand, proline is degraded into a glutamic acid by the two enzymes of a proline dehydrogenase (ProDH) and a P5C dehydrogenase.

When each of the aforesaid plants is subjected to a water stress (the state in which water is difficult to absorb) such as a high salinity stress or a drought stress, the expression level of the P5CS gene

5

is increased to activate the P5CS. However, the P5CR activity and the gene expression are constant at a low level. Further, the gene expression and the enzyme activity related to metabolism are also in the inhibited states. However, once the water stress has been removed, conversely, this time, the gene expression and enzyme activity related to biosynthesis are inhibited, so that the expression of the ProDH gene is rapidly induced, and the enzyme activity is also enhanced. As a result, the proline accumulated in the cytoplasm is rapidly metabolized to a glutamic acid.

From the foregoing description, it is considered that the P5CS becomes rate-limiting for proline synthesis under a water stress. Whereas, the ProDH becomes rate-limiting for proline metabolism after releasing the water stress (Yoshida et al., Plant Cell Physiol, 38: 1095 - 1102 (1997)).

SUMMARY OF THE INVENTION

It is predicted that food shortage due to an expansion of the saline soil area caused by drought and semi-drought with the deterioration of global environment, and population growth will become increasingly more serious in the future. Researches have been pursued in diversified fields respectively on the breeding of crop plants resistant to a high salinity stress, a drought stress, and a low temperature stress (the state in which water is

10

20

25

difficult to absorb) as those playing an important role in solving the world food problem, and the results are expected to be promising.

It is an object of the present invention to provide a rice plant which has a high proline accumulating ability, and accordingly has improved salinity-tolerance, drought-tolerance, and low temperature-tolerance by focusing attention on the importances of a Δ^{1} -pyrroline-5-carboxylate (P5C) synthetase (P5CS) and a proline dehydrogenase (ProDH) which are the rate-limiting enzymes related to synthesis and metabolism of proline in plants, and regulating the expression of genes for the enzymes with a gene recombination technology, and its production method.

The P5CS gene related to proline synthesis is introduced to be overexpressed; the antisense (reverse DNA sequence-containing) gene of the ProDH gene related to the metabolism is introduced to inhibit the degradation of proline; or both the P5CS gene and the antisense gene of the ProDH gene are introduced to promote the proline synthesis while inhibiting the degradation of proline. As a result, proline is accumulated with a high concentration in the cells of rice and a rice plant.

In the present invention, by accumulation of proline at a high concentration, it becomes possible to perform molecular breeding of rice and a rice plant

10

15

20

25

having salinity-tolerance, drought-tolerance, or low temperature-tolerance.

Heretofore, there is known no report that an increase in concentration of proline as an osmoprotectant is allowed by synthesis promotion and degradation inhibition in rice and a rice plant. inventors of the present invention have focused attention on the importances of the P5CS gene and the ProDH gene. Then, in order to solve novel technical problems which have not been known in the prior art, they have conducted studies from various fields including the study on the selection of the rice variety into which the gene is easily introduced, the study for improving the callus formation rate, the study on the construction of a vector for introducing the gene for rice, and the like. In consequence, they have provided novel technical elucidation, resulting in the completion of the present invention.

In the present invention, there are provided a rice plant transformed by introducing therein the proline synthesis gene and the antisense gene of the proline metabolism gene derived from rice or Arabidopsis thaliana individually or in combination, and its production method.

In the rice plant of the present invention, either or both of the gene encoding the synthetase protein of proline which is one of amino acids and the antisense gene of the proline dehydrogenage have been

10

15

20

25

introduced. With this construction, it is possible to implement a rice plant having improved salinity—tolerance, drought—tolerance, and low temperature—tolerance. Further, the mature rice seeds gathered from the rice plant of the present invention, particularly the rice seeds are characterized by keeping a high proline accumulating ability over a plurality of generations.

Further, the present invention is targeted for rice and rice plants. The targets have no particular restriction as long as they are the plants belonging to the rice plants. Examples of the plants belonging to the rice plants include rice, corn, wheat, barley, rye, turf, millet, and barn grass. In particular, the present invention can be more preferably applied to rice.

BRIEF DESCRIPTION OF THE DRAWINGS

FIGS. 1A to 1D are diagrams respectively showing the vectors for rice in which proline synthesis-related enzyme P5CS genes and proline metabolism-related enzyme ProDH genes, and antisense genes thereof have been respectively incorporated;

FIG. 2 is a graph showing the amount of proline accumulated in rice lines under no stress in which the vectors shown in FIGS. 1A to 1D have been respectively introduced by genetic engineering; and

FIG. 3 is a graph showing the salinity-

25

tolerance of each of the transgenic rice lines in which the proline-related genes have been respectively incorporated shown in FIG. 2.

5 DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

In rice plants of examples of the present invention, either or both of the proline (osmoprotectant) synthesis gene and the antisense gene of the proline motabolism derived from rice or Arabidopsis thaliana gene have been introduced for transformation.

Examples of one type of gene to be introduced to the rice plants of the examples of the present invention include: (1) a P5CS (Δ^1 -pyrroline-5-carboxylate (P5C) synthetase) gene of rice containing the sequence (DNA sequence and amino acid sequence) according to SEQ ID No. 1; (2) a P5CS (Δ^1 -pyrroline-5-carboxylate (P5C) synthetase) gene of Arabidopsis thaliana containing the sequence (DNA sequence and amino acid sequence) according to SEQ ID N2; and (3) the antisense (reverse DNA sequence-containing) gene of the ProDH (proline dehydrogenase) gene of Arabidopsis thaliana containing the sequence (DNA sequence and amino acid sequence) according to Seq ID NO. 3.

Examples of the two types of genes to be introduced into the rice plants of the examples of the present invention include:

(1) Two genes of the P5CS (Δ^1 -pyrroline-5-carboxylate

25

5

(P5C) synthetase) of rice containing the sequence according to SEQ ID NO. 1 or the P5CS gene of Arabidopsis thaliana containing the sequence according to SEQ ID NO. 2, and the antisense (reverse DNA sequence-containing) gene of the ProDH (proline dehydrogenase) gene of Arabidopsis thaliana containing the sequence according to SEQ ID NO. 3; and (2) Tandemly connected two genes of the P5CS (Δ^{1} -pyrroline-5-carboxylate (P5C) synthetase) gene of rice containing the sequence according to SEQ ID NO. 1 or the P5CS gene of Arabidopsis thaliana containing the sequence according to SEQ ID NO. 2, and the antisense (reverse DNA sequence-containing) gene of the ProDH (proline dehydrogenase) gene of Arabidopsis thaliana containing the sequence according to SEQ ID NO. 3.

In each of the vectors to be used in the examples of the present invention, there is incorporated any one gene of the P5CS (Δ^1 -pyrroline-5-carboxylate (P5C) synthetase) gene of rice containing the sequence according to SEQ ID NO. 1, the P5CS gene of Arabidopsis thaliana containing the sequence according to SEQ ID NO. 2, and the antisense (reverse DNA sequence-containing) gene of the ProDH (proline dehydrogenase) gene of Arabidopsis thaliana containing the sequence according to SEQ ID NO. 3. Alternatively, there are incorporated two genes of the P5CS gene of rice or Arabidopsis thaliana, and the aforesaid antisense gene in tandemly connected relation to each

25

other.

The rice plants of the examples of the present invention can be obtained by, for example, any of the following methods.

- 5 (1) The aforesaid vector is introduced into the calli derived from a rice plant, and the calli are grown. Then, a plant body is regenerated from the calli;
 - (2) The aforesaid vector is introduced into the protoplast derived from a rice plant, and a plant body is regenerated from the colony obtained by growing the protoplast; and
 - (3) Crossing with the rice plants obtained by introducing the vector therein by genetic engineering is carried out.

Examples of the production method of the rice plants of the examples of the present invention include the following methods:

- (1) The aforesaid vector is introduced into the calliderived from a rice plant by using Agrobacterium tumefaciens, and the calli are grown. Then, a plant body is regenerated from the calli;
- (2) The aforesaid vector is introduced into the protoplast derived from a rice plant by electroporation, and a plant body is regenerated from the colony obtained by growing the protoplast; and
- (3) Crossing with the rice plants obtained by introducing the vector therein by genetic engineering is carried out.

10

20

25

These production methods provide a rice plant having a high proline accumulating ability, and having improved salinity-tolerance, drought-tolerance, and low temperature-tolerance levels.

Further, mature seeds gathered from the rice plants of the examples of the present invention, particularly the rice seeds will maintain their high proline accumulating abilities over a plurality of generations.

The rice plants of the examples of the present invention and its production method will be described in details by way of embodiments thereof by using rice as a typical example step by step below. It is needless to say that the steps described below are applicable to other rice plants than rice with or without changing the various conditions.

(Gene cloning)

First, a mRNA is extracted from a rice seedling. A cDNA is synthesized by using the mRNA. The cDNA is combined with a vector made of a plasmid or a phage, and introduced into E. coli to prepare a recombinant The resulting transformant in which the recombinant DNA has been introduced is subjected to screening by plaque hybridization using the P5CS gene from Arabidopsis thaliana as a probe. The sequences of the P5CS genes from rice and Arabidopsis thaliana have been already reported (Yoshiba et al., Plant J. (1995) 7:751-760, and Igarashi et al., Plant Mol. Biol. (1997)

10

15

20

25

33:857-865). Based on these reports, appropriate primers are designed, and subjected to screening by PCR to select a target transformant. A target plasmid is isolated from the transformant obtained. If required, it is cut with an appropriate restriction enzyme, and subjected to subcloning in a plasmid vector for cloning. It is also possible to subject the P5CS gene of Arabidopsis thaliana to cloning in the same manner as with rice. However, as a sample from which a mRNA is to be extracted, the one subjected to a high salinity stress (immersed in a 250 mM NaCl solution or the like) or the one subjected to a drought stress treatment is more preferable than the one bred under a normal environment. This is because the P5CS gene is induced in response to a water stress such as a high salinity stress or a drought stress (Yoshiba et al., Plant J. (1995) 7: 751-760, Igarashi et al., Plant Mol. Biol. (1997) 33: 857-865, and Yoshiba et al., Plant Cell Physiol. (1997) 38: 1095-1102).

On the other hand, it is also possible to subject the ProDH gene of Arabidopsis thaliana (its sequence has already been reported in Kiyosue et al., Plant Cell (1996) 8:1323-1335) to cloning in the foregoing manner. However, as the sample from which a mRNA is to be extracted, there may be used the one which has been subjected to a drought stress (about 10-hour treatment), then immersed in water again, and allowed to absorb water, the one which has been

10

15

20

25

immersed in a proline solution, and allowed to absorb proline, or the like. This is due to the following fact. Namely, the ProDH gene is inhibited from its expression under a water stress, and the gene expression is induced by a high concentration of proline (Kiyosue et al., Plant Cell (1996) 8: 1323-1335, and Yoshiba et al., Plant Cell Physiol. (1997) 38: 1095-1102).

If the samples as described above are used, it is possible to isolate the P5CS gene and the ProDH gene not only from rice or Arabidopsis thaliana but also from other rice plants.

(Construction of gene introduction vector)

Respective P5CS genes and ProDH genes subjected to cloning are cut from plasmids with appropriate restriction enzymes, and, as shown in FIGS. 1A to 1D, each is combined behind the 35S promoter of a cauliflower mosaic virus of a vector for rice obtained by modifying a pBI vector. In FIGS. 1A to 1D, RB denotes the right border, 35SPro denotes the promoter of a cauliflower mosaic virus, P5CS denotes the proline synthesis—related enzyme gene of rice or Arabidopsis thaliana, ProDH denotes proline metabolism—related enzyme gene of Arabidopsis thaliana, Noster denotes the terminator of a nopaline synthetase gene, HTP denotes a hygromycine resistant gene, and LB denotes the left border. Whereas, each of the arrows indicates the orientation of the sense of each gene.

25

5

In FIGS. 1A to 1D, FIG. 1A is a diagram showing an example of the vector (construct) so constructed that the sequence in the order of RB-35SPro-P5CS-Noster-35SPro-HTP-Noster-LB has been achieved. FIG. 1B is a diagram showing an example in which, with respect to FIG. 1A, the same sequence in the order of RB-35SPro-P5CS-Noster-35SPro-HTP-Noster-LB as in the construct of FIG. 1A has been achieved, but the gene P5CS has been sequenced in antisense orientation. FIG. 1C is a diagram showing an example in which the gene ProDH has been sequenced in antisense orientation, and substituted for the gene P5CS of the construct of FIG. 1A, to construct a vector with a sequence in the order of RB-35SPro-ProDH (antisense)-Noster-35SPro-HTP-Noster-LB. FIG. 1D is a diagram showing an example in which, to the construct of FIG. 1A, the gene ProDH has been further sequenced in antisense orientation, and the construct shown in FIG. 1C has been further connected thereto in tandem, to construct a vector with a sequence in the order of RB-35SPro-P5CS-Noster-35SPro-ProDH (antisense)-Noster-35SPro-HTP-Noster-LB.

The 35S promoter is well known as a promoter which is strong and invariably induces the gene expression in any tissue. As for the orientation in which the gene is incorporated, the P5CS gene is connected in the sense orientation, and the ProDH gene in the antisense orientation.

Then, each vector to which each of the genes

25

5

has been connected is introduced into Agrobacterium tumefaciens EHA 101 by electroporation. The Agrobacterium tumefaciens in which each construct (FIGS 1A to 1D) has been introduced is cultured and grown in a YEP medium containing Bacto Pepton (10 g/l), Bacto Yeast Extract (10 q/l), sodium chloride (5 q/l), 1M magnesium chloride (2 ml/l), and hygromycine B (50 mg/l) at 28 $^{\circ}$ C. Gene introduction is carried out by infecting the callus cell of rice with the Agrobacterium tumefaciens into which each construct (FIGS. 1A - 1D) has been introduced. The construct D is so designed that the two genes (the P5CS gene and the ProDH gene) are connected to each other in tandem to be simultaneously introduced. However, even if the constructs A and C are mixed for coinfection, it is also possible obtain the same effects as with the construct D.

Incidentally, a HPT (hygromycine resistant) gene is connected to each construct. This is for efficiently selecting the cell and plant body transformed for the basic research on analysis of the effects of the introduced genes. Therefore, the HPT gene is not required to be incorporated therein for actual cultivation on the salt damaged land or the dry land.

(Induction of rice calli for gene introduction)

Mature rice seeds are sterilized with 70 %

ethyl alcohol for 10 minutes, and with 3 % sodium

25

5

hypochlorite for 1 hour after stripping the hulls therefrom. After sterilization, the seeds are washed with sterilized water 3 times, and bedded on a pH 5.8 N6 medium (2N6 medium) containing 1 g/l casamino acid, 30 g/l sucrose, 2 mg/l 2,4-dichlorophenoxyacetic acid, and 2 g/l Gelrite, and cultured at 28 $^{\circ}$ C in the dark for 3 to 5 weeks.

(Gene introduction into rice calli)

Out of the rice calli induced in the foregoing manner, the ones with a size of 1 to 3 mm are bedded on the 2N6 medium again, and cultured at 28 $^{\circ}$ C in the dark for 3 to 4 days. As a result, it is possible to enhance the division activity of the callus cell. The gene introduction is carried out by mixing the cultured calli and a solution of each construct-introduced Agrobacterium tumefaciens grown in the YEP medium (the solution diluted so that the concentration of the bacteria is 0.1 as determined at OD 660nm) for infection. Thereafter, the calli are cultured at 25 $^{\circ}$ C in the dark for 3 days. After cultivation, the calli are washed and sterilized several times by a cefotaxime aqueous solution with a concentration of 1 mg/4 ml to remove extra bacteria attached to the surfaces of the calli, and cleaned with a sterilized kim towel or the like. Subsequently, it is bedded on a 2N6 medium (secondary selection medium) containing 250 mg/l cefotaxime and 10 mg/l hygromycine B, and cultured at 28 °C in the dark for 1 week.

10

15

20

25

(Selection of transformed calli and regeneration of plant body)

The calli cultured in the medium containing cefotaxime is bedded on a medium (secondary selection medium) in which the content of hygromycine B has been increased to 30 mg/l, and cultured at 28 $^{\circ}\mathrm{C}$ in the dark for 3 weeks. Thereafter, the calli are transferred to a pH 5.8 MS medium (regeneration induction medium) containing 30 g/l sucrose, 30 g/l sorbitol, 2 g/l casamino acid, 11 g/l MES buffer, 2 mg/l NAA, 1 mg/l kinetin, 250 mg/l cefotaxime, 30 mg/l hygromycine B, and 4 g/l Gelrite, and cultured in the bright place at 28 $^{\circ}\mathrm{C}$ for 3 week. The gene-introduced calli form a green spot, from which shoots and roots are regenerated. The regenerated calli are further transferred to a pH 5.8 MS medium (plant body formation medium) containing 30 g/l sucrose, 250 mg/l cefotaxime, 30 mg/l hygromycine B, and 8 g/l agar, from which plant hormones have been removed, and cultured in the bright place at 28 $^{\circ}$ C for several weeks. In consequence, the plant body is bred more largely.

(Breeding of transformed rice plant body and seed formation)

Upon having grown to a seedling height of about 4 to 5 cm in a petri dish, the regenerated rice is transferred to a planter in which the soil for raising seedling is placed. Then, it is bred in an artificial climate system with an illuminance of about 20,000 lx

25

5

under a temperature condition of 28 °C until the fourth leaf to the fifth leaf develop. Subsequently, the seedling is further transferred into a pot containing the soil into which a fertilizer has been appropriately added, and bred in a greenhouse until the seeds ripen. Assuming that the present generation of the plant body regenerated is of the TO generation, and that the seeds obtainable from this plant body is of the T1 generation, the ones of the T2 to T3 generations are bred. When they are cultivated in an actual farm land, they are required to be commercialized after carrying out the various safety evaluation tests over further generations, and confirming the safety.

(Extraction of proline from transformed rice and concentration measurement thereof)

Proline is extracted from the leaves of the seedling (whose forth leaf has developed) of the transformed rice of the T2 generation or the T3 generation. The leaves of the rice seedling bred in the artificial climate system are cut off in an amount of about 200 mg by scissors or the like. Then, in a mortar, liquid nitrogen is added thereto, and the leaves are ground into powder. The resulting sample in powder form is mixed with pure water, and further milled by means of a homogenizer or the like. The milled sample is heated at 97 $^{\circ}$ C for 6 minutes, and then ice cooled. The sample is then centrifuged at about 17,000 $^{\circ}$ G for 10 minutes at 4 $^{\circ}$ C to separate the

25

5

supernatant. To the supernatant obtained, a trichloroacetic acid is added and mixed so that the final concentration is 5 %. The resulting mixture is then centrifuged at about 17,000 ×G for 10 minutes at 4 °C again to precipitate protein. Proline as an osmoprotectant is contained in the supernatant at this step, and the concentration thereof is determined by means of high performance liquid chromatography (HPLC). The qualitative determination of proline is carried out in the following manner. The solutions in which various amino acids have been dissolved to a given concentration are previously determined by HPLC. The amount of proline contained in the leaf of an actual transgenic rice is determined based on the retention times.

FIG. 2 shows the proline content of each of the transgenic rice lines under no stress into which various genes have been introduced. The hollow graphs in the leftmost column represent control samples into which proline-related genes have not been incorporated. Whereas, the solidly shaded graphs in the right-hand five columns denote respective transgenic rice lines into which proline-related genes have been incorporated. It is indicated that the proline content varies according to the type of the gene introduced.

There is observed almost no accumulation for each sample in which the P5CS gene (OsP5CS) of rice has been introduced in antisense orientation (FIG. 1B) in

10

20

25

the second column from left. For each sample in which the P5CS gene (AtP5CS) of Arabidopsis thaliana has been introduced in sense orientation (FIG. 1A) in the third column from left, there is observed an increase in amount of proline accumulated over the control samples. Similarly, for each sample in which the ProDH gene (AtProDH) of Arabidopsis thaliana has been introduced in antisense orientation (FIG. 1C) and each sample in which the P5CS gene (OsP5CS) of rice has been introduced in sense orientation (FIG. 1A) in the fourth and fifth columns from left, respectively, there are observed increases in amount of proline accumulated over the control sample. In contrast to these, for each sample in which the P5CS gene (OsP5CS) of rice has been introduced in sense orientation, and the ProDH gene (AtProDH) of Arabidopsis thaliana in antisense orientation in the rightmost column, there is observed a considerably larger amount of proline accumulated (100 times or more with respect to the control sample for the case where the amount of proline accumulated is larger) as compared with each of the aforesaid samples in which one type of gene has been introduced. it is indicated that each sample of OsP5CS (in the fifth column from left) is slightly more effective for proline accumulation than each sample of AtP5CS (in the third column from left) among the samples in which genes have been introduced in sense orientation.

(Salinity tolerance test and improvement of

25

5

salinity tolerance of transgenic rice)

FIG. 3 shows the results of a salinity tolerance test performed at a 250 mM concentration (about half the salt concentration of sea water) by using several lines of the transgenic rice for which proline accumulation has been observed shown in the right hand four columns of FIG. 2. The hollow graphs denote the control samples in which proline related genes have not been incorporated. Whereas, the solidly shaded graphs denote the transgenic rice samples. The salinity tolerance test was carried out in accordance with the testing method using known survival rates as indexes (Japanese Published Unexamined Patent Application No. Hei 09-266726, title of the invention: evaluation of salt resistance of plant). It has been shown that the control samples in which proline-related genes have not been introduced die 5 days after a salt treatment, while the transgenic rice samples which accumulate proline show high survival rates, i.e., 95 % for the third day, and 65 % even after the five-day treatment. This indicates that the salinity tolerance can be improved by transforming rice, and thereby enhancing the proline accumulating ability thereof.

Therefore, if the gramineous crop produced according to the present invention is subjected to breeding by further pursuing detailed analysis such as the safety evaluation thereon, it becomes capable of being cultured in the salt accumulated soil or the

desertified soil. Therefore, food productivity can be expected to be improved. Further, it can be largely expected that the crop plant is also capable of coping with the population growth in developing countries.

In accordance with the present invention, it has become possible to produce a transgenic rice plant having an enhance proline accumulating ability.

Further, for the rice plant produced by the method of the present invention, the amount of proline accumulated therein has been increased, so that it has become possible to improve the salinity tolerance level thereof.

[Sequence Listing]

<110> Hitachi, LTD.

RIKEN

Japan International Research Center for Agricaltural Science

Bio-oriented Technology Research

Advancement Institute (BRAIN) <120> Transgenic rice plant and its family with environmental stress resistant by proline accumulation of high level and its production.

<130> NT01P0353

<160> 3

<210> 1

<211> 2549

<212> DNA

<213> Oryza sativa L.

<220>

<221> CDS

<222> 99..2249

<300>

<301> Yumiko Igarashi, Yoshu Yoshiba, Yukika Sanada, Kazuko Yamaguchi-Shinozaki, Keishiro Wada, Kazuo Shinozaki

<302> Characterization of the gene for Δ ¹-pyrroline-5-carboxylate synthetase and correlation between the expression of the gene and salt tolerance in *Oryza sativa* L.

<303> Plant Molecular biology

< 30	4>	33														
< 30	6>	857	-86	5												
< 30	7>	199	6-1	2-0	3											
< 30	8>	D49	714													
< 30	9>	199	5-0	3-1	6											
<40	0 >	1														
gcgg	gctgo	egg o	eggca	aaggo	cg go	gaga	acgt	g gga	agagg	ggat	ttad	caggi	tag a	aggga	agaggg	60
tgga	ngga	gga g	gaggo	ctgag	gg ct	tagga	aagcg	g gti	ttcg	cc at	g go	cg ag	gc g1	tc ga	ac ccg	116
										Me	et Al	la Se	er Va	al As	sp Pro	
											1			Ę	5	
tcc	coo	agc	ttc	øt.ø	ឧទទ	gac	gt.g	aag	cgc	gt.c	atc	atc	ลลฐ	gt.g	ggc	164
		Ser														
			10	,	8		,	15	0				20			
act	gca	gtt	gtc	tcc	aga	caa	gat	gga	aga	ttg	gct	ttg	ggc	agg	gtt	212
Thr	Ala	Val	Val	Ser	Arg	Gln	Asp	Gly	Arg	Leu	Ala	Leu	Gly	Arg	Val	
		25					30					35				
																0.00
		ctg														260
Gly		Leu	Cys	Glu	Gln		Lys	Glu	Leu	Asn		Leu	Gly	Tyr	Glu	
	40					45					50					
gtg	att	ttg	gtc	acc	tca	ggt	gct	gtt	gga	gtg	ggg	cga	cag	cga	ctt	308
Val	Ile	Leu	Val	Thr	Ser	Gly	Ala	Val	Gly	Val	Gly	Arg	Gln	Arg	Leu	
55					60					65					70	

agg	tac	cgg	aag	ctt	gtc	aat	agc	agc	ttt	gct	gat	ctg	caa	aag	cca	356
Arg	Tyr	Arg	Lys	Leu	Val	Asn	Ser	Ser	Phe	Ala	Asp	Leu	Gln	Lys	Pro	
				75					80					85		
cag	atg	gag	tta	gat	gga	aag	gct	tgt	gcc	gct	gtt	ggt	cag	agt	gga	404
Gln	Met	Glu	Leu	Asp	Gly	Lys	Ala	Cys	Ala	Ala	Val	Gly	Gln	Ser	Gly	
			90					95					100			
ctg	atg	gct	ctt	tac	gat	atg	ttg	ttt	aac	caa	ctg	gat	gtc	tcg	tca	452
Leu	Met	Ala	Leu	Tyr	Asp	Met	Leu	Phe	Asn	Gln	Leu	Asp	Val	Ser	Ser	
		105					110					115				
tct	caa	ctt	ctt	gtc	acc	gac	agt	gat	ttt	gag	aac	cca	aag	ttc	cgg	500
Ser	Gln	Leu	Leu	Val	Thr	Asp	Ser	Asp	Phe	Glu	Asn	Pro	Lys	Phe	Arg	
	120					125					130					
						gtt										548
	Gln	Leu	Thr	Glu		Val	Glu	Ser	Leu		Asp	Leu	Lys	Val		
135					140					145					150	
						gat										596
Pro	Ile	Phe	Asn		Asn	Asp	Ala	Ile			Arg	Lys	Ala		Tyr	
				155					160					165		
																0.4.4
						ttc										644
Glu	Asp	ser		Gly	TIE	Phe	ırp		Asn	Asp	Ser	Leu		GLY	Leu	
			170					175					180			

ttg	gca	ctg	gaa	ctg	aaa	gct	gat	ctc	ctt	att	ctg	ctc	agt	gat	gtg	692
Leu	Ala	Leu	Glu	Leu	Lys	Ala	Asp	Leu	Leu	Ile	Leu	Leu	Ser	Asp	Val	
		185					190					195				
gat	ggg	ttg	tat	agt	ggt	cca	cca	agt	gaa	cca	tca	tca	aaa	atc	ata	740
Asp	Gly	Leu	Tyr	Ser	Gly	Pro	Pro	Ser	Glu	Pro	Ser	Ser	Lys	Ile	Ile	
	200					205					210					
cac	act	tat	att	aaa	gaa	aag	cat	cag	caa	gaa	atc	act	ttt	gga	gac	788
His	Thr	Tyr	Ile	Lys	G1u	Lys	His	G1n	Gln	Glu	Ile	Thr	Phe	Gly	Asp	
215					220					225					230	
aaa	tct	cgt	gta	ggt	aga	gga	ggc	atg	aca	gca	aaa	gtg	aag	gct	gct	836
Lys	Ser	Arg	Val	Gly	Arg	Gly	Gly	Met	Thr	Ala	Lys	Val	Lys	Ala	Ala	
				235					240					245		
gtc	ttg	gct	tca	aat	agc	ggc	aca	cct	gtg	gtt	att	aca	agt	ggg	ttt	884
Val	Leu	Ala	Ser	Asn	Ser	Gly	Thr	Pro	Val	Val	Ile	Thr	Ser	Gly	Phe	
			250					255					260			
gaa	aat	cgg	agc	att	ctt	aaa	gtt	ctt	cat	ggg	gaa	aaa	att	ggt	act	932
Glu	Asn	Arg	Ser	Ile	Leu	Lys	Val	Leu	His	G1y	Glu	Lys	Ile	Gly	Thr	
		265					270					275				
ctc	ttt	cac	aag	aat	gcg	aat	ttg	tgg	gaa	tca	tct	aag	gat	gtt	agt	980
Leu	Phe	His	Lys	Asn	Ala	Asn	Leu	Trp	Glu	Ser	Ser	Lys	Asp	Val	Ser	
	280					285					290					

act	cgt	gag	atg	gct	gtt	gcc	gca	aga	gat	tgt	tca	agg	cat	cta	cag	1028
Thr	Arg	Glu	Met	Ala	Val	Ala	Ala	Arg	Asp	Cys	Ser	Arg	His	Leu	Gln	
295					300					305					310	
aat	ttg	tca	tca	gag	gaa	cga	aaa	aag	ata	ttg	cta	gat	gtt	gca	gat	1076
Asn	Leu	Ser	Ser	Glu	Glu	Arg	Lys	Lys	Ile	Leu	Leu	Asp	Val	Ala	Asp	
				315					320					325		
gct	ttg	gag	gca	aat	gag	gat	tta	ata	agg	tct	gag	aat	gaa	gct	gat	1124
Ala	Leu	Glu	Ala	Asn	Glu	Asp	Leu	Ile	Arg	Ser	Glu	Asn	Glu	Ala	Asp	
			330					335					340			
gta	gct	gcg	gcc	caa	gtt	gct	gga	tat	gag	aag	cct	ttg	gtt	gct	aga	1172
Val	Ala	Ala	Ala	Gln	Val	Ala	Gly	Tyr	Glu	Lys	Pro	Leu	Val	Ala	Arg	
		345					350					355				
ttg	act	ata	aaa	cca	gga	aag	ata	gca	agc	ctt	gca	aaa	tct	att	cgt	1220
Leu	Thr	Ile	Lys	Pro	Gly	Lys	Ile	Ala	Ser	Leu	Ala	Lys	Ser	Ile	Arg	
	360					365					370					
acc	ctt	gca	aat	atg	gaa	gac	cct	ata	aac	cag	ata	ctt	aaa	aag	aca	1268
Thr	Leu	Ala	Asn	Met	Glu	Asp	Pro	Ile	Asn	Gln	Ile	Leu	Lys	Lys	Thr	
375					380					385					390	
					tta											1316
Glu	Val	Ala	Asp		Leu	Val	Leu	Glu		Thr	Ser	Cys	Pro		Gly	
				395					400					405		

gtt	ctc	tta	att	gtt	ttt	gag	tcc	cga	cct	gat	gcc	ttg	gtt	cag	att	1364
Val	Leu	Leu	Ile	Val	Phe	Glu	Ser	Arg	Pro	Asp	Ala	Leu	Val	Gln	Ile	
			410					415					420			
gca	tct	ttg	gca	att	cga	agt	ggt	aat	ggt	ctt	ctc	cta	aaa	ggt	gga	1412
Ala	Ser	Leu	Ala	Ile	Arg	Ser	Gly	Asn	Gly	Leu	Leu	Leu	Lys	Gly	Gly	
		425					430					435				
aaa	gaa	gct	atc	aga	tca	aac	acg	ata	ttg	cat	aag	gtt	ata	act	gat	1460
Lys	Glu	Ala	Ile	Arg	Ser	Asn	Thr	Ile	Leu	His	Lys	Val	Ile	Thr	Asp	
	440					445					450					
gct	att	cct	cgt	aat	gtt	ggt	gaa	aaa	ctt	att	ggc	ctt	gtt	aca	act	1508
Ala	Ile	Pro	Arg	Asn	Val	Gly	Glu	Lys	Leu	Ile	Gly	Leu	Val	Thr	Thr	
455					460					465					470	
aga	gat	gag	atc	gca	gat	ttg	cta	aag	ctt	gat	gat	gtc	att	gat	ctt	1556
Arg	Asp	Glu	Ile	Ala	Asp	Leu	Leu	Lys	Leu	Asp	Asp	Val	Ile	Asp	Leu	
				475					480					485		
gtc	act	cca	aga	gga	agt	aat	aag	ctt	gtc	tct	caa	atc	aag	gcg	tca	1604
Val	Thr	Pro	Arg	Gly	Ser	Asn	Lys	Leu	Val	Ser	Gln	Ile	Lys	Ala	Ser	
			490					495					500			
act	aag	att	cct	gtt	ctt	ggg	cat	gct	gat	ggt	ata	tgc	cac	gta	tat	1652
Thr	Lys	Ile	Pro	Val	Leu	Gly	His	Ala	Asp	Gly	Ile	Cys	His	Val	Tyr	
		505					510					515				

att	gac	aaa	tca	gct	gac	atg	gat	atg	gca	aaa	ctt	att	gta	atg	gat	1700
Ile	Asp	Lys	Ser	Ala	Asp	Met	Asp	Met	Ala	Lys	Leu	Ile	Val	Met	Asp	
	520					525					530					
gca	aaa	act	gat	tac	cca	gca	gcc	tgc	aat	gca	atg	gag	acc	tta	cta	1748
Ala	Lys	Thr	Asp	Tyr	Pro	Ala	Ala	Cys	Asn	Ala	Met	Glu	Thr	Leu	Leu	
535					540					545					550	
gtt	cat	aag	gat	ctt	atg	aag	agt	cca	ggc	ctt	gac	gac	ata	tta	gta	1796
Val	His	Lys	Asp	Leu	Met	Lys	Ser	Pro	Gly	Leu	Asp	Asp	Ile	Leu	Val	
				555					560					565		
gca	cta	aaa	aca	gaa	gga	gtt	aat	att	tat	ggt	gga	cct	att	gcg	cac	1844
Ala	Leu	Lys	Thr	Glu	Gly	Val	Asn	Ile	Tyr	Gly	Gly	Pro	Ile	Ala	His	
			570					575					580			
aaa	gct	ctg	gga	ttt	cca	aaa	gct	gtt	tca	ttt	cat	cat	gag	tat	agt	1892
Lys	Ala	Leu	Gly	Phe	Pro	Lys	Ala	Val	Ser	Phe	His	His	Glu	Tyr	Ser	
		585					590					595				
tct	atg	gcc	tgc	act	gtt	gag	ttt	gtt	gat	gat	gtt	caa	tca	gca	att	1940
Ser	Met	Ala	Cys	Thr	Val	Glu	Phe	Val	Asp	Asp	Val	Gln	Ser	Ala	Ile	
	600					605					610					
gac	cat	att	cat	cgt	tat	gga	agt	gct	cat	aca	gat	tgt	atc	gtc	act	1988
Asp	His	Ile	His	Arg	Tyr	Gly	Ser	Ala	His	Thr	Asp	Cys	Ile	Val	Thr	
615					620					625					630	

aca	gat	gat	aag	gta	gca	gag	act	ttt	cta	cgc	aga	gtt	gat	agt	gct	2036
Thr	Asp	Asp	Lys	Val	Ala	Glu	Thr	Phe	Leu	Arg	Arg	Val	Asp	Ser	Ala	
				635					640					645		
gct	gta	ttt	cat	aat	gca	agt	acg	aga	ttc	tct	gat	ggg	gct	cgt	ttt	2084
Ala	Val	Phe	His	Asn	Ala	Ser	Thr	Arg	Phe	Ser	Asp	Gly	Ala	Arg	Phe	
			650					655					660			
																0.1.0.0
	_													gcc		2132
Gly	Leu		Ala	Glu	Val	Gly		Ser	Thr	Gly	Arg	lle	His	Ala	Arg	
		665					670					675				
											_			ttg	•	2180
Gly		Val	Gly	Val	Glu	Gly	Leu	Leu	Thr	Thr	Arg	Trp	Ile	Leu	Arg	
	680					685					690					
														acc		2228
	Arg	Gly	Gln	Val	Val	Asn	Gly	Asp	Lys	Asp	Val	Val	Tyr	Thr	His	
695					700					705					710	
	,															
		ctt				tgag	ggtca	aaa t	gcto	cttt	it ag	gcctg	gttca	1		2276
Lys	Ser	Leu	Pro		Gln											
				715												
	-4		_4_4	4 4			,									0000
ggag	uagg	gig a	iatat	cett	t ta	agaa	ıtgga	ı ttg	acta	ictt	tatt	ttgt	ca t	cttg	gtacaa	2336
gcat	ctts	ntt o	rraan	atto	າດ ຜລ	tora	1++2+	t os	++++	aaa	aat+		act t	+000	atgtg	2206
2001	, , , , , , ,	۶ باب	, 550	uuul	√u ga	ugga	ıııal	, ugc	いいいしし	రకర	5566	\cdot	いししし	lucab	ia i K l K	4050

acaccaaaaa taaattcatc agttctgaga gcaagatttt ggaggttcag cttctccatg 2456 taataagtaa attcagttct gagaacttgt gtaccaacgc gctatgttgc ttgtaatgag 2516

2549

<210> 2

<211> 2571

<212> DNA

<213> Arabidopsis thaliana

cgatactaac atctgtgatt gcacatatac taa

<220>

<221> CDS

<222> 107...2260

<301> Yoshu Yoshiba, Tomohiro Kiyasue, Takeshi Katagiri, Hiroko

Ueda, Tsuyoshi Mizoguchi, Kazuko Yamaguchi-Shinozaki, Keishiro

Wada, Yoshinori Harada, Kazuo Shinozaki

 $\langle 302 \rangle$ Correlation between the induction of a gene for Δ^{1-} pyrroline-5-carboxylate synthetase and the accumulation of proline in *Arabidopsis thaliana* under osmotic stress.

<303> The Plant Journal

<304> 7

<305> 5

<306> 751-760

<307> 1995-01-20

<308> D32138

<309> 1994-07-12

<400> 2

ctgatattta ttttcttacc ttaaatacga cggtgcttca ctgagtccga ctcagttaac 60

tcgt	tcct	ct o	ctctg	gtgtg	gt gg	gttt1	tggta	a gao	egace	gacg	acga					115
												Λ	Met (Glu (ilu	
													1			
cta	gat	cgt	tca	cgt	gct	ttt	gcc	aga	gac	gtc	aaa	cgt	atc	gtc	gtt	163
Leu	Asp	Arg	Ser	Arg	Ala	Phe	Ala	Arg	Asp	Val	Lys	Arg	Ile	Val	Val	
	5					10					15					
aag	gtt	ggg	aca	gca	gtt	gtt	act	gga	aaa	ggt	gga	aga	ttg	gct	ctt	211
Lys	Val	Gly	Thr	Ala	Val	Val	Thr	Gly	Lys	Gly	Gly	Arg	Leu	Ala	Leu	
20					25					30					35	
ggt	cgt	tta	gga	gca	ctg	tgt	gaa	cag	ctt	gcg	gaa	tta	aac	tcg	gat	259
Gly	Arg	Leu	Gly	Ala	Leu	Cys	Glu	Gln	Leu	Ala	Glu	Leu	Asn	Ser	Asp	
				40					45					50		
gga	ttt	gag	gtg	ata	ttg	gtg	tca	tct	ggt	gcg	gtt	ggt	ctt	ggc	agg	307
					Leu											
- J			55					60				,	65	J	Ü	
саа	agg	ctt	cet	tat	cga	caa	t.t.a	gtc	aat.	agc	agc	ttt	aca	gat.	ctt	355
					Arg											
0111	111 S	70	111 6	1,11	2111 8	0.111	75		11011	501	501	80	2124	пор	Dou	
		10					10					00				
റമന	220	cct	car	act	സമര	c++	as+	aaa	ລລຕ	act	† a †	act	aa+	a++	ແແລ	403
					gaa					_		_				±∪€
GIN		rro	GIN	ınr	Glu		ASP	ату	LYS	ALA		кта	дТΆ	val	σιу	
	85					90					95					

caa	agc	agt	ctt	atg	gct	tac	tat	gag	act	atg	ttt	gac	cag	ctt	gat	451
Gln	Şer	Ser	Leu	Met	Ala	Tyr	Tyr	Glu	Thr	Met	Phe	Asp	Gln	Leu	Asp	
100					105					110					115	
gtg	acg	gca	gct	caa	ctt	ctg	gtg	aat	gac	agt	agt	ttt	aga	gac	aag	499
Val	Thr	Ala	Ala	G1n	Leu	Leu	Val	Asn	Asp	Ser	Ser	Phe	Arg	Asp	Lys	
				120					125					130		
gat	ttc	agg	aag	caa	ctt	aat	gaa	act	gtc	aag	tct	atg	ctt	gat	ttg	547
Asp	Phe	Arg	Lys	G1n	Leu	Asn	Glu	Thr	Val	Lys	Ser	Met	Leu	Asp	Leu	
			135					140					145			
agg	gtt	att	cca	att	ttc	aat	gag	aat	gat	gct	att	agc	acc	cga	aga	595
Arg	Val	Ile	Pro	Ile	Phe	Asn	Glu	Asn	Asp	Ala	Ile	Ser	Thr	Arg	Arg	
		150					155					160				
gcc	cca	tat	cag	gat	tct	tct	ggt	att	ttc	tgg	gat	aac	gat	agc	tta	643
Ala	Pro	Tyr	Gln	Asp	Ser	Ser	Gly	Ile	Phe	Trp	Asp	Asn	Asp	Ser	Leu	
	165					170					175					
gct	gct	cta	ctg	gcg	ttg	gaa	ctg	aaa	gct	gat	ctt	ctg	att	ctt	ctg	691
Ala	Ala	Leu	Leu	Ala	Leu	Glu	Leu	Lys	Ala	Asp	Leu	Leu	Ile	Leu	Leu	
180					185					190					195	
agc	gat	gtt	gaa	ggt	ctt	tac	aca	ggc	cct	cca	agt	gat	cct	aac	tca	739
Ser	Asp	Val	Glu	Gly	Leu	Tyr	Thr	Gly	Pro	Pro	Ser	Asp	Pro	Asn	Ser	
				200					205					210		

aag	ttg	atc	cac	act	ttt	gtt	aaa	gaa	aaa	cat	caa	gat	gag	att	aca	787
Lys	Leu	Ile	His	Thr	Phe	Val	Lys	Glu	Lys	His	Gln	Asp	Glu	Ile	Thr	
			215					220					225			
ttc	ggc	gac	aaa	tca	aga	tta	ggg	aga	ggg	ggt	atg	act	gca	aaa	gtc	835
Phe	G1y	Asp	Lys	Ser	Arg	Leu	Gly	Arg	Gly	Gly	Met	Thr	Ala	Lys	Val	
		230					235					240				
aaa	gct	gca	gtc	aat	gca	gct	tat	gct	ggg	att	cct	gtc	atc	ata	acc	883
Lys	Ala	Ala	Val	Asn	Ala	Ala	Tyr	Ala	Gly	Ile	Pro	Val	Ile	Ile	Thr	
	245					250					255					
agt	ggg	tat	tca	gct	gag	aac	ata	gat	aaa	gtc	ctc	aga	gga	cta	cgt	931
Ser	Gly	Tyr	Ser	Ala	Glu	Asn	Ile	Asp	Lys	Val	Leu	Arg	Gly	Leu	Arg	
260					265					270					275	
gtt	gga	acc	ttg	ttt	cat	caa	gat	gct	cgt	tta	tgg	gct	ccg	atc	aca	979
Val	Gly	Thr	Leu	Phe	His	Gln	Asp	Ala	Arg	Leu	Trp	Ala	Pro	Ile	Thr	
				280					285					290		
gat	tct	aat	gct	cgt	gac	atg	gca	gtt	gct	gcg	agg	gaa	agt	tcc	aga	1027
Asp	Ser	Asn	Ala	Arg	Asp	Met	Ala	Val	Ala	Ala	Arg	Glu	Ser	Ser	Arg	
			295					300					305			
aag	ctt	cag	gcc	tta	tct	tcg	gaa	gac	agg	aaa	aaa	att	ctg	ctt	gat	1075
Lys	Leu	Gln	Ala	Leu	Ser	Ser	Glu	Asp	Arg	Lys	Lys	Ile	Leu	Leu	Asp	
		310					315					320				

att	gee	oat	gee	ctt	gaa	gca	aat.	øt.t.	act	aca	atc	ลลล	gct	gag	aat	1123
														Glu		
116		nsp	пта	Lou	oru	330	71511	141	1111	1111	335	2,5	1114	OI u	71011	
	325					330					JJJ					
				í	4				4					4	-4-	1171
											_			tca		1171
Glu	Leu	Asp	Val	Ala		Ala	Gin	Glu	Ala		Leu	Glu	Glu	Ser		
340					345					350					355	
gtg	gct	cgc	tta	gtt	atg	aca	cct	gga	aag	atc	tcg	agc	ctt	gca	gct	1219
Val	Ala	Arg	Leu	Val	Met	Thr	Pro	Gly	Lys	Ile	Ser	Ser	Leu	Ala	Ala	
				360					365					370		
tca	gtt	cgt	aag	cta	gct	gat	atg	gaa	gat	cca	atc	ggc	cgt	gtt	tta	1267
Ser	Val	Arg	Lys	Leu	Ala	Asp	Met	Glu	Asp	Pro	Ile	Gly	Arg	Val	Leu	
			375					380					385			
aag	aaa	aca	gag	gtg	gca	gat	ggt	ctt	gtc	tta	gag	aag	acc	tca	tca	1315
Lys	Lys	Thr	Glu	Val	Ala	Asp	Gly	Leu	Val	Leu	Glu	Lys	Thr	Ser	Ser	
		390					395					400				
cca	tta	ggc	gta	ctt	ctg	att	gtt	ttt	gaa	tcc	cga	cct	gat	gca	ctt	1363
														Ala		
	405	,				410	,				415					
	100					110					-10					
a+2	000	2+0	ac+	tes	c++	acc	2+0	cat	ant	aus	22+	au+	c++	ctg	cta	1411
																T.ITT
	Q1IJ	тте	ита	ser		uig	тте	ur 8	Ser.		USII	GIA	Leu	Leu		
420					425					430					435	

aag	ggt	gga	aag	gag	gcc	cgg	cga	tca	aat	gct	atc	tta	cac	aag	gtg	1459
Lys	Gly	Gly	Lys	Glu	Ala	Arg	Arg	Ser	Asn	Ala	Ile	Leu	His	Lys	Val	
				440					445					450		
o to	oo+	an t	gan.	2++	000	non	act	a++	aaa	aat	222	ctc	att	ຕກລ	ctt	1507
														gga		1001
116	ınr	Asp		116	Pro	GIU	ınr		GIÀ	GIÀ	Lys	Leu		Gly	Leu	
			455					460					465			
gtg	act	tca	aga	gaa	gag	att	cct	gat	ttg	ctt	aag	ctt	gat	gac	gtt	1555
Val	Thr	Ser	Arg	Glu	Glu	Ile	Pro	Asp	Leu	Leu	Lys	Leu	Asp	Asp	Val	
		470					475					480				
atc	gat	ctt	gtg	atc	cca	aga	gga	agc	aac	aag	ctt	gtt	act	cag	ata	1603
Ile	Asp	Leu	Val	Ile	Pro	Arg	Gly	Ser	Asn	Lys	Leu	Val	Thr	Gln	Ile	
	485					490					495					
aaa	aat	act	aca	aaa	atc	cct	gtg	cta	ggt	cat	gct	gat	gga	atc	tgt	1651
Lys	Asn	Thr	Thr	Ļys	Ile	Pro	Val	Leu	Gly	His	Ala	Asp	Gly	Ile	Cys	
500					505					510					515	
cat	gta	tat	gtc	gac	aag	gct	tgt	gat	acg	gat	atg	gca	aag	cgc	ata	1699
His	Val	Tyr	Val	Asp	Lys	Ala	Cys	Asp	Thr	Asp	Met	Ala	Lys	Arg	Ile	
				520					525					530		
gtt	tct	gat	gca	aag	ttg	gac	tat	cca	gca	gcc	tgt	aat	gcg	atg	gaa	1747
Val	Ser	Asp	Ala	Lys	Leu	Asp	Tyr	Pro	Ala	Ala	Cys	Asn	Ala	Met	Glu	
			535					540					545			

		ctt														1795
Thr	Leu	Leu	Val	His	Lys	Asp		Glu	Gln	Asn	Ala		Leu	Asn	Glu	
		550					555					560				
ctt	att	ttt	act	cto	cag	age	aat	០០១	gtc	act	t.t.σ	tat	ggt.	gga	сса	1843
		Phe													_	1010
Dou	565	1110	1114	Dou	0111	570	11011	01)	142	1111	575	~,-	0-7	023		
agg	gca	agt	aag	ata	ctg	aac	ata	cca	gaa	gca	cgg	tca	ttc	aac	cat	1891
Arg	Ala	Ser	Lys	Ile	Leu	Asn	Ile	Pro	Glu	Ala	Arg	Ser	Phe	Asn	His	
580					585					590					595	
gag	tac	tgt	gcc	aag	gct	tgc	act	gtt	gaa	gtt	gta	gaa	gac	gtt	tat	1939
Glu	Tyr	Cys	Ala	Lys	Ala	Cys	Thr	Val	Glu	Val	Val	Glu	Asp	Val	Tyr	
				600					605					610		
ggt	gct	ata	gat	cac	att	cac	cga	cat	ggg	agt	gca	cac	aca	gac	tgc	1987
Gly	Ala	Ile	Asp	His	Ile	His	Arg	His	Gly	Ser	Ala	His	Thr	Asp	Cys	
			615					620					625			
		aca								_		_				2035
Ile	Val	Thr	Glu	Asp	His	Glu		Ala	Glu	Leu	Phe		Arg	Gln	Val	
		630					635					640				
										_			4			2002
		gct						_					_			2083
Asp		Ala	Ala	Val	Phe		Asn	Ala	Ser	Inr		rne	Ser	Asp	GIY	
	645					650					655					

ttc	cga	ttt	gga	ctt	ggt	gca	gag	gtg	ggg	gta	agc	acg	ggc	agg	atc	2131
Phe	Arg	Phe	Gly	Leu	Gly	Ala	Glu	Val	Gly	Val	Ser	Thr	Gly	Arg	Ile	
660					665					670					675	
cat	gct	cgt	ggt	cca	gtc	ggg	gtc	gaa	gga	tta	ctt	aca	acg	aga	tgg	2179
His	Ala	Arg	Gly	Pro	Val	Gly	Val	Glu	Gly	Leu	Leu	Thr	Thr	Arg	Trp	
				680					685					690		
ata	atg	aga	gga	aaa	gga	caa	gtt	gtc	gac	gga	gac	aat	gga	att	gtt	2227
Ile	Met	Arg	Gly	Lys	Gly	G1n	Val	Val	Asp	Gly	Asp	Asn	Gly	Ile	Val	
			695					700					705			
tac	acc	cat	cag	gac	att	ссс	atc	caa	gct	taaa	acaag	gac 1	ttcc	gagtg	gt	2277
Tyr	Thr	His	Gln	Asp	Ile	Pro	Ile	G1n	Ala							
		710					715									
gtgt	ttgt	gt a	atttg	gttg	ga ga	acttg	gagga	ı gaş	gacac	aga	ggag	ggatg	ggg (ctttt	ttgtt	2337
tcct	ctct	gc 1	ttagt	acto	a ta	itcct	atca	ı tta	attat	tat	tact	tacta	act ·	tatta	ittgaa	2397
acco	tcgc	ett a	atgta	igtgg	gt tt	tgat	ttag	g ggt	tagg	gatt	gcad	ccaaa	aaa ·	taaga	tccac	2457
ttta	ccac	ett a	agtct	tgct	c at	aagt	acga	ı tga	agaa	cat	ttaa	attag	gct ·	tctct	tcttg	2517
tcat	tgta	ag o	ctacc	taca	ıc at	ttct	gato	ttt	atca	aga	tact	acta	ict -	tttc		2571

```
<210> 3
```

<211> 1833

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> 113...1612

<301> Tomohiro Kiyasue, Yoshu Yoshiba, Kazuko Yamaguchi-Shinozaki, Kazuo Shinozaki

<302>Title : A nuclear gene encoding mitochondrial
prolne dehydrogenase, an enzyme involved in
proline metabolism, is upregulated by proline but

downregulated by dehydration in Arabidopsis.

<303> The Plant Cell

<304> 8

<306> 1323-1335

<307> 1996-05-27

<308> D83025

<309> 1995-12-25

<400> 3

agcgtttaga aaaaaacagc gataaaaccg aaacatcaag caaacaaaaa aaaaagagaa 60

gagaaattat tttttttgt tttcgttttc aaaaacaaaa tctttgaatt tt atg gca 118
Met Ala

1

acc cgt ctt ctc cga aca aac ttt atc cgg cga tct tac cgt tta ccc 166
Thr Arg Leu Leu Arg Thr Asn Phe Ile Arg Arg Ser Tyr Arg Leu Pro

_	4.0	1 -
5	10	15
J	10	10

gct	ttt	agc	ccg	gtg	ggt	cct	ccc	acc	gtg	act	gct	tcc	acc	gcc	gtc	214
Ala	Phe	Ser	Pro	Val	Gly	Pro	Pro	Thr	Val	Thr	Ala	Ser	Thr	Ala	Val	
	20					25					30					
gtc	ccg	gag	att	ctc	tcc	ttt	gga	caa	caa	gca	ccg	gaa	cca	cct	ctt	262
Val	Pro	Glu	Ile	Leu	Ser	Phe	Gly	Gln	Gln	Ala	Pro	Glu	Pro	Pro	Leu	
35					40					45					50	
cac	cac	cca	aaa	ccc	acc	gag	caa	tct	cac	gat	ggt	ctc	gat	ctc	tcc	310
His	His	Pro	Lys	Pro	Thr	Glu	Gln	Ser	His	Asp	Gly	Leu	Asp	Leu	Ser	
				55					60					65		
gat	caa	gcc	cgt	ctt	ttc	tcc	tct	atc	cca	acc	tct	gat	ctc	ctc	cgt	358
Asp	Gln	Ala	Arg	Leu	Phe	Ser	Ser	Ile	Pro	Thr	Ser	Asp	Leu	Leu	Arg	
			70					75					80			
tcc	acc	gcc	gtg	ttg	cat	gcg	gcg	gcg	ata	ggt	cct	atg	gtc	gac	cta	406
Ser	Thr	Ala	Val	Leu	His	Ala	Ala	Ala	Ile	Gly	Pro	Met	Val	Asp	Leu	
		85					90					95				
ggg	acg	tgg	gtc	atg	agc	tct	aaa	ctt	atg	gac	gct	tcg	gtg	acg	cgt	454
Gly	Thr	Trp	Val	Met	Ser	Ser	Lys	Leu	Met	Asp	Ala	Ser	Val	Thr	Arg	
	100					105					110					
ggc	atg	gtt	tta	ggg	ctt	gtg	aaa	agt	acg	ttt	tat	gac	cat	ttt	tgc	502
Gly	Met	Val	Leu	Gly	Leu	Val	Lys	Ser	Thr	Phe	Tyr	Asp	His	Phe	Cys	

115					120					125					130	
														gtt Val		550
	·		-	135					140					145		
gaa	gct	act	ggt	ctt	aaa	ggg	atg	ctt	gtc	tat	ggc	gtc	gaa	cac	gcc	598
Glu	Ala	Thr	G1y	Leu	Lys	Gly	Met	Leu	Val	Tyr	Gly	Val	Glu	His	Ala	
			150					155					160			
gat	gac	gct	gta	tct	tgt	gat	gat	aac	atg	caa	caa	ttc	att	cga	acc	646
Asp	Asp	Ala	Val	Ser	Cys	Asp	Asp	Asn	Met	Gln	Gln	Phe	Ile	Arg	Thr	
		165					170					175				
						4.4.			+ - +		+++	0.00	+00	art a	c++	694
														gtg Val		034
116		Ата	АТА	Lys	Ser.	185	rro	1111	Set	urs	190	Sei	Set	Val	Vai	
	180					100					150					
gtg	aag	ata	act	gcc	att	tgt	cca	att	agt	ctt	ctg	aaa	cga	gtg	agc	742
Val	Lys	Ile	Thr	Ala	Ile	Cys	Pro	Ile	Ser	Leu	Leu	Lys	Arg	Val	Ser	
195					200					205					210	
gat	ctg	ctg	cgg	tgg	gaa	tac	aaa	agt	ccg	aac	ttc	aaa	ctc	tca	tgg	790
														Ser		
				215					220					225		
																000
														tac		838
Lys	Leu	Lys	Ser	Phe	Pro	Val	Phe	Ser	Glu	Ser	Ser	Pro	Leu	Tyr	His	

230	235	240

aca	aac	tca	gaa	ccg	gaa	ccg	tta	acc	gcg	gaa	gaa	gaa	agg	gag	ctc	886
Thr	Asn	Ser	Glu	Pro	Glu	Pro	Leu	Thr	Ala	Glu	Glu	Glu	Arg	Glu	Leu	
		245					250					255				
gaa	gca	gct	cat	gga	agg	att	caa	gaa	atc	tgt	agg	aaa	tgc	caa	gag	934
Glu	Ala	Ala	His	Gly	Arg	Ile	Gln	Glu	Ile	Cys	Arg	Lys	Cys	Gln	Glu	
	260					265					270					
tcc	aat	gta	cca	ttg	ttg	att	gat	gcg	gaa	gac	aca	atc	ctc	caa	ccc	982
Ser	Asn	Val	Pro	Leu	Leu	Ile	Asp	Ala	Glu	Asp	Thr	Ile	Leu	Gln	Pro	
275					280					285					290	
gcg	atc	gat	tac	atg	gct	tat	tca	tcg	gcg	atc	atg	ttc	aat	gct	gac	1030
Ala	Ile	Asp	Tyr	Met	Ala	Tyr	Ser	Ser	Ala	Ile	Met	Phe	Asn	Ala	Asp	
				295					300					305		
aaa	gac	cga	cca	atc	gtt	tac	aac	acg	att	cag	gcg	tac	ttg	aga	gac	1078
Lys	Asp	Arg	Pro	Ile	Val	Tyr	Asn	Thr	Ile	Gln	Ala	Tyr	Leu	Arg	Asp	
			310					315					320			
gcc	ggt	gag	aga	ctg	cat	ttg	gca	gta	caa	aat	gct	gag	aaa	gag	aat	1126
Ala	G1y	Glu	Arg	Leu	His	Leu	Ala	Val	Gln	Asn	Ala	Glu	Lys	Glu	Asn	
		325					330					335				
	•															
gtt	cct	atg	ggg	ttc	aag	ttg	gtg	aga	ggg	gct	tac	atg	tct	agc	gaa	1174
Val	Pro	Met	Gly	Phe	Lys	Leu	Val	Arg	Gly	Ala	Tyr	Met	Ser	Ser	Glu	

340 345 350

cgt	agc	ttg	gcg	gat	tcc	ctg	ggt	tgc	aag	tcg	cca	gtc	cac	gac	aca	1222
Arg	Ser	Leu	Ala	Asp	Ser	Leu	Gly	Cys	Lys	Ser	Pro	Val	His	Asp	Thr	
355					360					365					370	
att	cag	gat	act	cac	tet	t.øt.	tac	aat.	gat.	t.øt.	atø	aca	ttc	ctø	atø	1270
		Asp														12.0
110	OIII	иор	1111		001	Cys	1 7 1	11011		Oys	NIC C	1111	1 110	385	MCC	
				375					380					300		
gag	aaa	gca	tca	aac	ggt	tct	ggt	ttc	ggt	gtc	gtt	ctc	gca	aca	cat	1318
Glu	Lys	Ala	Ser	Asn	Gly	Ser	Gly	Phe	Gly	Val	Val	Leu	Ala	Thr	His	
			390					395					400			
220	act	gat	tea	aaa	ana	ctt	aca	tea	ກກຂ	222	aca	aat	020	ctc	aaa	1366
																1300
ASII	Ala	Asp	Set	Gly	AIg	Leu		Set	MIG	LyS	нта		ASP	Leu	GIY	
		405					410					415				
atc	gat	aaa	cag	aac	ggg	aag	ata	gag	ttt	gca	cag	cta	tat	ggt	atg	1414
Ile	Asp	Lys	Gln	Asn	Gly	Lys	Ile	Glu	Phe	Ala	Gln	Leu	Tyr	Gly	Met	
	420					425					430					
tea	nat	gca	++ a	tee	++0	aaa	++2	220	ລຕລ	സമ	aaa	++0	aat	at t	200	1462
																1402
	ASP	Ala	Leu	ser		СТА	Leu	Lys	Arg		GTÀ	Pne	ASN	vaı		
435					440					445					450	
aag	tac	atg	ccg	ttt	gga	ссс	gtc	gca	acc	gct	ata	ccg	tat	ctt	ctc	1510
Lys	Tyr	Met	Pro	Phe	Gly	Pro	Val	Ala	Thr	Ala	Ile	Pro	Tyr	Leu	Leu	

cga	cgc	gct	tat	gag	aac	cgg	gga	atg	atg	gcc	acc	gga	gct	cat	gac	1558
Arg	Arg	Ala	Tyr	Glu	Asn	Arg	Gly	Met	Met	Ala	Thr	Gly	Ala	His	Asp	
			470					475					480			
cgt	caa	ctc	atg	agg	atg	gaa	ctt	aag	agg	aga	tta	atc	gcc	ggg	att	1606
Arg	Gln	Leu	Met	Arg	Met	Glu	Leu	Lys	Arg	Arg	Leu	Ile	Ala	Gly	Ile	
		485					490					495				
gcg	taaa	agaga	aga g	gtatg	ggago	cc at	taaa	atgaa	a ati	tggga	aaat	gtag	gatga	aat		1659
Ala																
aaa	tttc	ttc ·	tatgt	tagti	tt aa	agaaa	attga	a aaa	acaaa	aaaa	ttat	taata	ata a	agaaa	atggag	1719

taggtaagaa catttcctgt ggctaaatat ttttcatgag ggactatgtt tttactatca 1779

atatatcatt cacaaatgta tattcacctt atcaataaaa atgctttta cttt